PCT10

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            RAW SEQUENCE LISTING                 DATE: 02/25/2002
            PATENT APPLICATION:  US/10/049,137   TIME: 11:46:51

            Input Set : A:\Pklseq1.app
            Output Set: N:\CRF3\02252002\J049137.raw

   3 <110> APPLICANT: Ogas, Joseph P.
   4        Somerville, Christopher R.
   6 <120> TITLE OF INVENTION: Methods and Compositions for Regulating Developmental
   7        Identity
   9 <130> FILE REFERENCE: 7024-473
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/049,137
  13 <141> CURRENT FILING DATE: 2000-08-18
  15 <150> PRIOR APPLICATION NUMBER: US 60/149,975
  17 <151> PRIOR FILING DATE: 1999-08-20
  19 <160> NUMBER OF SEQ ID NOS: 30
  21 <170> SOFTWARE: MS Notebook
  23 <210> SEQ ID NO: 1
  25 <211> LENGTH: 4177
  27 <212> TYPE: DNA
  29 <213> ORGANISM: Arabidopsis thaliana
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  33 <400> SEQUENCE: 1
  34 atg agt agt ttg gtg gag agg ctt cgc ata cga tct gat agg aaa cca      48
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  36  1               5                  10                  15
  38 gtt tat aac cta gat gat tct gat gat gac gac ttc gtt cct aaa aaa      96
  39 Val Tyr Asn Leu Asp Asp Ser Asp Asp Asp Asp Phe Val Pro Lys Lys
  40              20                  25                  30
  42 gat cga acc ttt gag caa gtc gag gct att gtc aga act gat gcg aaa     144
  43 Asp Arg Thr Phe Glu Gln Val Glu Ala Ile Val Arg Thr Asp Ala Lys
  44          35                  40                  45
  46 gaa aat gca tgt cag gct tgt ggg gaa agt act aat ctt gta agc tgc     192
  47 Glu Asn Ala Cys Gln Ala Cys Gly Glu Ser Thr Asn Leu Val Ser Cys
  48      50                  55                  60
  50 aat aca tgc act tat gcg ttc cat gct aaa tgc tta gtt cca cct ctt     240
  51 Asn Thr Cys Thr Tyr Ala Phe His Ala Lys Cys Leu Val Pro Pro Leu
  52  65                  70                  75                  80
  54 aaa gat gct tcc gtg gaa aat tgg aga tgc cct gaa tgt gtt agt cct     288
  55 Lys Asp Ala Ser Val Glu Asn Trp Arg Cys Pro Glu Cys Val Ser Pro
  56              85                  90                  95
  58 ctt aac gag ata gat aag ata ttg gat tgt gaa atg cgt cct aca aaa     336
  59 Leu Asn Glu Ile Asp Lys Ile Leu Asp Cys Glu Met Arg Pro Thr Lys
  60             100                 105                 110
  62 tct agt gaa caa ggt tcc tcc gat gcg gaa ccg aag cca att ttt gtg     384
  63 Ser Ser Glu Gln Gly Ser Ser Asp Ala Glu Pro Lys Pro Ile Phe Val
  64          115                 120                 125
  66 aaa cag tat ctc gtg aag tgg aag gga tta tca tac ctt cac tgc tct     432
  67 Lys Gln Tyr Leu Val Lys Trp Lys Gly Leu Ser Tyr Leu His Cys Ser
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68      130                    135                    140
70 tgg gtg cct gag aag gag ttc cag aag gct tat aag tca aat cat cgt    480
71 Trp Val Pro Glu Lys Glu Phe Gln Lys Ala Tyr Lys Ser Asn His Arg
72 145                    150                    155                160
74 tta aaa acc aga gtg aac aat ttt cac cgt caa atg gag tca ttc aat    528
75 Leu Lys Thr Arg Val Asn Asn Phe His Arg Gln Met Glu Ser Phe Asn
76                    165                    170                    175
78 aac agc gaa gat gat ttt gtt gcc ata cgt cct gag tgg acc act gtt    576
79 Asn Ser Glu Asp Asp Phe Val Ala Ile Arg Pro Glu Trp Thr Thr Val
80                    180                    185                    190
82 gat cgg att ctt gcc tgc aga gag gaa gat ggg gag ctg gaa tat ctt    624
83 Asp Arg Ile Leu Ala Cys Arg Glu Glu Asp Gly Glu Leu Glu Tyr Leu
84          195                    200                    205
86 gtc aaa tat aaa gag cta tcc tat gat gaa tgt tat tgg gag tca gaa    672
87 Val Lys Tyr Lys Glu Leu Ser Tyr Asp Glu Cys Tyr Trp Glu Ser Glu
88      210                    215                    220
90 tca gac atc tca acc ttc cag aat gaa att caa agg ttc aag gat gta    720
91 Ser Asp Ile Ser Thr Phe Gln Asn Glu Ile Gln Arg Phe Lys Asp Val
92 225                    230                    235                240
94 aat tct aga act cgc aga agt aaa gat gtt gac cat aaa aga aat ccc    768
95 Asn Ser Arg Thr Arg Arg Ser Lys Asp Val Asp His Lys Arg Asn Pro
96                    245                    250                    255
98 aga gac ttt caa cag ttt gat cat act cct gaa ttc ctc aaa ggc ttg    816
99 Arg Asp Phe Gln Gln Phe Asp His Thr Pro Glu Phe Leu Lys Gly Leu
100                    260                    265                    270
102 tta cat cca tac cag ctt gag gga ctt aat ttt ttg cgg ttc tcg tgg   864
103 Leu His Pro Tyr Gln Leu Glu Gly Leu Asn Phe Leu Arg Phe Ser Trp
104          275                    280                    285
106 tca aaa cag acg cat gta atc ctt gct gat gaa atg gga cta ggc aag   912
107 Ser Lys Gln Thr His Val Ile Leu Ala Asp Glu Met Gly Leu Gly Lys
108      290                    295                    300
110 aca att caa agc att gcc ctt tta gct tca ctt ttt gag gag aac ctc   960
111 Thr Ile Gln Ser Ile Ala Leu Leu Ala Ser Leu Phe Glu Glu Asn Leu
112 305                    310                    315                320
114 att ccg cat ttg gta att gct cct cta tcg act ctg cgt aac tgg gag  1008
115 Ile Pro His Leu Val Ile Ala Pro Leu Ser Thr Leu Arg Asn Trp Glu
116                    325                    330                    335
118 aga gag ttt gcc aca tgg gcc cca cag atg aac gtg gtt atg tat ttt  1056
119 Arg Glu Phe Ala Thr Trp Ala Pro Gln Met Asn Val Val Met Tyr Phe
120          340                    345                    350
122 ggc act gcg caa gct cga gca gtt atc aga gaa cat gag ttt tac tta  1104
123 Gly Thr Ala Gln Ala Arg Ala Val Ile Arg Glu His Glu Phe Tyr Leu
124          355                    360                    365
126 tcg aaa gat caa aaa aag atc aag aaa aag aaa tct gga caa ata agt  1152
127 Ser Lys Asp Gln Lys Lys Ile Lys Lys Lys Ser Gly Gln Ile Ser
128      370                    375                    380
130 agc gaa agc aag caa aaa aga atc aag ttt gat gtc ctc ctc aca tcg  1200
131 Ser Glu Ser Lys Gln Lys Arg Ile Lys Phe Asp Val Leu Leu Thr Ser
132 385                    390                    395                400
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134 tat gag atg atc aac cta gat tca gca gtt cta aaa cca att aag tgg   1248
135 Tyr Glu Met Ile Asn Leu Asp Ser Ala Val Leu Lys Pro Ile Lys Trp
136             405                 410                 415
138 gag tgc atg att gtt gat gaa ggt cat cga ctg aaa aat aag gat tca   1296
139 Glu Cys Met Ile Val Asp Glu Gly His Arg Leu Lys Asn Lys Asp Ser
140             420                 425                 430
142 aag ctg ttc tct tca ttg aca cag tat tca agt aac cac cgt att ctt   1344
143 Lys Leu Phe Ser Ser Leu Thr Gln Tyr Ser Ser Asn His Arg Ile Leu
144             435                 440                 445
146 ctg aca gga aca cca ctt cag aac aac ttg gat gaa ctt ttc atg ctc   1392
147 Leu Thr Gly Thr Pro Leu Gln Asn Asn Leu Asp Glu Leu Phe Met Leu
148         450                 455                 460
150 atg cat ttt ctt gat gcg ggg aag ttt gga agt ttg gag gag ttc cag   1440
151 Met His Phe Leu Asp Ala Gly Lys Phe Gly Ser Leu Glu Glu Phe Gln
152 465                 470                 475                 480
154 gag gag ttc aaa gat att aat caa gag gag cag atc tca agg ttg cac   1488
155 Glu Glu Phe Lys Asp Ile Asn Gln Glu Glu Gln Ile Ser Arg Leu His
156             485                 490                 495
158 aaa atg ttg gct cca cat ttg ctc aga agg gta aaa aaa gac gta atg   1536
159 Lys Met Leu Ala Pro His Leu Leu Arg Arg Val Lys Lys Asp Val Met
160             500                 505                 510
162 aaa gac atg ccc ccc aaa aag gag ctc att ttg cgt gtt gat ctg agc   1584
163 Lys Asp Met Pro Pro Lys Lys Glu Leu Ile Leu Arg Val Asp Leu Ser
164             515                 520                 525
166 agt ctg cag aaa gaa tat tac aaa gct att ttt acc cgt aat tat caa   1632
167 Ser Leu Gln Lys Glu Tyr Tyr Lys Ala Ile Phe Thr Arg Asn Tyr Gln
168         530                 535                 540
170 gta ttg aca aaa aag gga ggt gct caa att tcc ctt aat aac att atg   1680
171 Val Leu Thr Lys Lys Gly Gly Ala Gln Ile Ser Leu Asn Asn Ile Met
172 545                 550                 555                 560
174 atg gaa tta cga aaa gta tgc tgc cat cct tat atg cta gag ggt gtt   1728
175 Met Glu Leu Arg Lys Val Cys Cys His Pro Tyr Met Leu Glu Gly Val
176             565                 570                 575
178 gag cca gtt att cac gac gca aat gaa gct ttc aaa caa ctt ttg gag   1776
179 Glu Pro Val Ile His Asp Ala Asn Glu Ala Phe Lys Gln Leu Leu Glu
180             580                 585                 590
182 tct tgt gga aag ctg caa ctt cta gat aaa atg atg gtc aaa ctg aaa   1824
183 Ser Cys Gly Lys Leu Gln Leu Leu Asp Lys Met Met Val Lys Leu Lys
184         595                 600                 605
186 gag caa gga cac aga gtc cta ata tac aca cag ttt cag cat atg ctg   1872
187 Glu Gln Gly His Arg Val Leu Ile Tyr Thr Gln Phe Gln His Met Leu
188         610                 615                 620
190 gac tta ctt gaa gac tac tgt acc cat aag aaa tgg cag tac gag cga   1920
191 Asp Leu Leu Glu Asp Tyr Cys Thr His Lys Lys Trp Gln Tyr Glu Arg
192 625                 630                 635                 640
194 att gat gga aag gtt ggc gga gct gag cgg caa ata cgc ata gat cgg   1968
195 Ile Asp Gly Lys Val Gly Gly Ala Glu Arg Gln Ile Arg Ile Asp Arg
196             645                 650                 655
198 ttc aat gcc aaa aat tct aac aag ttt tgt ttt ttg ctc tcc aca aga   2016
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199 Phe Asn Ala Lys Asn Ser Asn Lys Phe Cys Phe Leu Leu Ser Thr Arg
200          660          665          670
202 gct ggt ggc tta gga ata aat ctt gca acg gct gat aca gta atc att     2064
203 Ala Gly Gly Leu Gly Ile Asn Leu Ala Thr Ala Asp Thr Val Ile Ile
204      675          680          685
206 tat gac agt gac tgg aat cct cat gct gat ctt caa gca atg gct aga     2112
207 Tyr Asp Ser Asp Trp Asn Pro His Ala Asp Leu Gln Ala Met Ala Arg
208      690          695          700
210 gct cat cga ctt ggc caa aca aat aag gtg atg att tat agg ctc ata     2160
211 Ala His Arg Leu Gly Gln Thr Asn Lys Val Met Ile Tyr Arg Leu Ile
212 705          710          715          720
214 aac cga ggc acc att gaa gaa agg atg atg caa ttg act aaa aag aaa     2208
215 Asn Arg Gly Thr Ile Glu Glu Arg Met Met Gln Leu Thr Lys Lys Lys
216          725          730          735
218 atg gtt cta gag cat ctt gtt gtt ggg aaa ctc aaa aca caa aac att     2256
219 Met Val Leu Glu His Leu Val Val Gly Lys Leu Lys Thr Gln Asn Ile
220          740          745          750
222 aat cag gaa gag tta gat gac atc atc agg tat gga tca aag gag ctt     2304
223 Asn Gln Glu Glu Leu Asp Asp Ile Ile Arg Tyr Gly Ser Lys Glu Leu
224          755          760          765
226 ttt gct agt gaa gat gat gaa gca gga aag tct gga aaa att cat tat     2352
227 Phe Ala Ser Glu Asp Asp Glu Ala Gly Lys Ser Gly Lys Ile His Tyr
228     770          775          780
230 gat gat gcg gct ata gac aaa ttg ctt gat cgt gat ctc gtg gag gca     2400
231 Asp Asp Ala Ala Ile Asp Lys Leu Leu Asp Arg Asp Leu Val Glu Ala
232 785          790          795          800
234 gag gaa gtc tca gtg gat gat gaa gag gag aat gga ttc tta aag gct     2448
235 Glu Glu Val Ser Val Asp Asp Glu Glu Glu Asn Gly Phe Leu Lys Ala
236          805          810          815
238 ttc aag gtg gct aat ttt gaa tat ata gat gaa aat gag gca gca gca     2496
239 Phe Lys Val Ala Asn Phe Glu Tyr Ile Asp Glu Asn Glu Ala Ala Ala
240          820          825          830
242 tta gag gca cag aga gtc gct gct gaa agc aaa tct tca gca ggc aat     2544
243 Leu Glu Ala Gln Arg Val Ala Ala Glu Ser Lys Ser Ser Ala Gly Asn
244          835          840          845
246 tct gat aga gca agt tat tgg gaa gag ttg tta aaa gat aaa ttt gag     2592
247 Ser Asp Arg Ala Ser Tyr Trp Glu Glu Leu Leu Lys Asp Lys Phe Glu
248      850          855          860
250 ctg cac cag gct gag gag ctt aat gct ctt gga aaa agg aag aga agt     2640
251 Leu His Gln Ala Glu Glu Leu Asn Ala Leu Gly Lys Arg Lys Arg Ser
252 865          870          875          880
254 cgc aag cag ttg gta tcc att gaa gaa gat gat ctt gct ggt ttg gaa     2688
255 Arg Lys Gln Leu Val Ser Ile Glu Glu Asp Asp Leu Ala Gly Leu Glu
256          885          890          895
258 gat gtg agc tct gat gga gat gaa agt tat gaa gct gag tca aca gat     2736
259 Asp Val Ser Ser Asp Gly Asp Glu Ser Tyr Glu Ala Glu Ser Thr Asp
260          900          905          910
262 ggt gaa gca gca gga caa gga gtt cag acg ggt cga cgg ccg tac aga     2784
263 Gly Glu Ala Ala Gly Gln Gly Val Gln Thr Gly Arg Arg Pro Tyr Arg
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                  Input Set : A:\Pklseq1.app
                  Output Set: N:\CRF3\02252002\J049137.raw


264         915              920              925
266 aga aag ggt cgc gat aat ttg gaa cca act ccg ttg atg gaa ggt gag    2832
267 Arg Lys Gly Arg Asp Asn Leu Glu Pro Thr Pro Leu Met Glu Gly Glu
268     930              935              940
270 ggg aga tct ttc aga gta ctg ggt ttc aac cag agt caa agg gcc att    2880
271 Gly Arg Ser Phe Arg Val Leu Gly Phe Asn Gln Ser Gln Arg Ala Ile
272 945              950              955              960
274 ttt gta cag act ttg atg agg tat gga gct ggc aat ttt gat tgg aag    2928
275 Phe Val Gln Thr Leu Met Arg Tyr Gly Ala Gly Asn Phe Asp Trp Lys
276             965              970              975
278 gag ttt gtt cct cgc tta aag cag aag acc ttt gaa gaa ata aat gaa    2976
279 Glu Phe Val Pro Arg Leu Lys Gln Lys Thr Phe Glu Glu Ile Asn Glu
280             980              985              990
282 tat gga ata ctc ttc ttg aag cac att gct gaa gaa ata gac gag aat    3024
283 Tyr Gly Ile Leu Phe Leu Lys His Ile Ala Glu Glu Ile Asp Glu Asn
284             995             1000             1005
286 tct cca acc ttt tca gat ggt gtg ccc aag gaa gga ctt aga ata gaa    3072
287 Ser Pro Thr Phe Ser Asp Gly Val Pro Lys Glu Gly Leu Arg Ile Glu
288     1010            1015             1020
290 gat gtt cta gtc aga att gct ctt ctg ata cta gtt cag gag aag gtg    3120
291 Asp Val Leu Val Arg Ile Ala Leu Leu Ile Leu Val Gln Glu Lys Val
292 1025            1030             1035            1040
294 aaa ttt gta gaa gat cat cca ggg aaa cct gtt ttc ccc tct cgc att    3168
295 Lys Phe Val Glu Asp His Pro Gly Lys Pro Val Phe Pro Ser Arg Ile
296             1045             1050             1055
298 ctt gaa aga ttc ccc gga ctg aga agt gga aaa att tgg aag gag gaa    3216
299 Leu Glu Arg Phe Pro Gly Leu Arg Ser Gly Lys Ile Trp Lys Glu Glu
300             1060             1065             1070
302 cat gac aag ata atg ata cgt gct gtt tta aag cat ggg tac gga cgg    3264
303 His Asp Lys Ile Met Ile Arg Ala Val Leu Lys His Gly Tyr Gly Arg
304         1075             1080             1085
306 tgg caa gct att gtt gat gac aaa gag ttg ggg atc caa gag ctt atc    3312
307 Trp Gln Ala Ile Val Asp Asp Lys Glu Leu Gly Ile Gln Glu Leu Ile
308     1090             1095             1100
310 tgc aaa gaa ttg aat ttc cct cac ata agt ttg tct gct gct gaa caa    3360
311 Cys Lys Glu Leu Asn Phe Pro His Ile Ser Leu Ser Ala Ala Glu Gln
312 1105            1110             1115            1120
314 gct ggt ttg cag ggg cag aat ggt agt ggg ggc tct aat ccg gga gca    3408
315 Ala Gly Leu Gln Gly Gln Asn Gly Ser Gly Gly Ser Asn Pro Gly Ala
316             1125             1130             1135
318 cag act aac cag aat cct gga agc gtt att act ggg aac aat aat gct    3456
319 Gln Thr Asn Gln Asn Pro Gly Ser Val Ile Thr Gly Asn Asn Asn Ala
320             1140             1145             1150
322 tct gct gat ggg gct caa gta aac tcg atg ttc tat tat cgg gac atg    3504
323 Ser Ala Asp Gly Ala Gln Val Asn Ser Met Phe Tyr Tyr Arg Asp Met
324         1155             1160             1165
326 cag aga cga ctt gtt gag ttt gtg aaa aag cga gtt ctg ctt ttg gag    3552
327 Gln Arg Arg Leu Val Glu Phe Val Lys Lys Arg Val Leu Leu Leu Glu
328     1170             1175             1180
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

→

VERIFICATION SUMMARY   DATE: 02/25/2002
PATENT APPLICATION: US/10/049,137   TIME: 11:46:53

Input Set : **A:\Pklseql.app**
Output Set: **N:\CRF3\02252002\J049137.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4